SEQUENCE LISTING

<110> Università degli Studi di Roma "La Sapienza"
Consiglio Nazionale delle Ricerche

<120> Purification, cloning and biochemical characterization of XendoU, endoribonucleasic activity involved in Xenopus laevis small nuclear RNA splicing independent biosynthesis

<130> PCT25390

<150> IT RM2002A000365
<151> 2002-07-08

<160> 9

<170> PatentIn version 3.2

<210> 1
<211> 1265
<212> DNA
<213> Xenopus laevis

<220>
<221> misc_feature
<222> (1)..(38)
<223> 5' untranslated DNA region

<220>
<221> exon
<222> (39)..(915)

<220>
<221> terminator
<222> (916)..(918)

<220>
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<222> (916)..(1265)
<223> 3' untranslated DNA region

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attggggaac tgggagcaga gagtgacggg caggagcc atg gcg agt aac agg ggg 56
Met Ala Ser Asn Arg Gly
1 5

cag ctg aac cat gaa ctc tcc aag ctg ttt aat gag ctg tgg gac gca 104
Gln Leu Asn His Glu Leu Ser Lys Leu Phe Asn Glu Leu Trp Asp Ala
10 15 20

gat cag aac cgg atg aag tcc ggg aag gat tat cgg atc tcc ttg cag 152
Asp Gln Asn Arg Met Lys Ser Gly Lys Asp Tyr Arg Ile Ser Leu Gln
25 30 35

ggt aaa gca ggg tac gta ccc gcc ggt tcc aac cag gcc agg gac agc 200
Gly Lys Ala Gly Tyr Val Pro Ala Gly Ser Asn Gln Ala Arg Asp Ser

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    40                  45                  50

gcc tcg ttc ccg ctc ttc cag ttc gtc gat gag gag aag ctg aag agc      248
Ala Ser Phe Pro Leu Phe Gln Phe Val Asp Glu Glu Lys Leu Lys Ser
55              60                  65                  70

agg aag acg ttt gca acc ttc att tcc ctg ctg gac aat tat gag atg      296
Arg Lys Thr Phe Ala Thr Phe Ile Ser Leu Leu Asp Asn Tyr Glu Met
                75                  80                  85

gac acg ggg gtg gcc gag gtt gtg act ccg gag gaa atc gct gaa aac      344
Asp Thr Gly Val Ala Glu Val Val Thr Pro Glu Glu Ile Ala Glu Asn
            90                  95                  100

aac aac ttc ctg gac gcc att ctg gaa acc aaa gtg atg aag atg gca      392
Asn Asn Phe Leu Asp Ala Ile Leu Glu Thr Lys Val Met Lys Met Ala
        105                 110                 115

cat gac tac ctg gtg agg aag aac caa gcc aaa ccc acc cgg aat gac      440
His Asp Tyr Leu Val Arg Lys Asn Gln Ala Lys Pro Thr Arg Asn Asp
    120                 125                 130

ttc aag gtc caa ctg tac aac atc tgg ttc cag ctg tac tca cgg gcc      488
Phe Lys Val Gln Leu Tyr Asn Ile Trp Phe Gln Leu Tyr Ser Arg Ala
135                 140                 145                 150

cca ggg agc aga ccc gat tcg tgc ggc ttt gag cac gtg ttt gtg gga      536
Pro Gly Ser Arg Pro Asp Ser Cys Gly Phe Glu His Val Phe Val Gly
                155                 160                 165

gaa tcg aag cga ggg cag gag atg atg ggg ctt cac aac tgg gtc cag      584
Glu Ser Lys Arg Gly Gln Glu Met Met Gly Leu His Asn Trp Val Gln
            170                 175                 180

ttt tac ctt cag gag aag agg aag aac atc gac tat aaa gga tac gtg      632
Phe Tyr Leu Gln Glu Lys Arg Lys Asn Ile Asp Tyr Lys Gly Tyr Val
        185                 190                 195

gct cgg cag aac aag agt cgg ccg gat gaa gat gat cag gtg ttg aac      680
Ala Arg Gln Asn Lys Ser Arg Pro Asp Glu Asp Asp Gln Val Leu Asn
    200                 205                 210

ctg cag ttc aat tgg aag gag atg gtg aaa ccc gtc ggc agc agc ttc      728
Leu Gln Phe Asn Trp Lys Glu Met Val Lys Pro Val Gly Ser Ser Phe
215                 220                 225                 230

att ggc gtc agc ccg gaa ttc gaa ttc gcc ctt tac acc atc gtc ttc      776
Ile Gly Val Ser Pro Glu Phe Glu Phe Ala Leu Tyr Thr Ile Val Phe
                235                 240                 245

ctc gcg tct cag gag aag atg agc cga gaa gtc gtt cgg ctg gaa gaa      824
Leu Ala Ser Gln Glu Lys Met Ser Arg Glu Val Val Arg Leu Glu Glu
            250                 255                 260

tac gaa ctg cag atc gtc gtc aat cgc cac ggc cgt tat ata ggg acc      872
Tyr Glu Leu Gln Ile Val Val Asn Arg His Gly Arg Tyr Ile Gly Thr
        265                 270                 275
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gcc tac ccc gtc ctc ctg agc acc aat aac ccg gat ctg tac t            915
Ala Tyr Pro Val Leu Leu Ser Thr Asn Asn Pro Asp Leu Tyr
    280                 285                 290

gaggggggcgg ggctagagat cacagccggt tcccacggtt tgggtgcatt tactaacaaa   975

actgcaccaa tgcaacaatg caagcagata atgggggcag gtccatatcc ctctgctttc   1035

cctagcgtgt gtggggcaca ttaaccctat aactgtcact cactgcacca gacccattat   1095

ttaaccccac aagggacatc aagccagtgc cttgttatga gagagcgcag ccggggcttc   1155

tctactgtga aacttctgta ttgtatagag tttacttggt ttcttcctcc agacaatttc   1215

actttttttt tgctttgcct ttaaccatta aaagtccatg acatttctgt              1265
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<210> 2
<211> 292
<212> PRT
<213> Xenopus laevis

<400> 2

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Met Ala Ser Asn Arg Gly Gln Leu Asn His Glu Leu Ser Lys Leu Phe
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Asn Glu Leu Trp Asp Ala Asp Gln Asn Arg Met Lys Ser Gly Lys Asp
            20                  25                  30

Tyr Arg Ile Ser Leu Gln Gly Lys Ala Gly Tyr Val Pro Ala Gly Ser
        35                  40                  45

Asn Gln Ala Arg Asp Ser Ala Ser Phe Pro Leu Phe Gln Phe Val Asp
    50                  55                  60

Glu Glu Lys Leu Lys Ser Arg Lys Thr Phe Ala Thr Phe Ile Ser Leu
65                  70                  75                  80

Leu Asp Asn Tyr Glu Met Asp Thr Gly Val Ala Glu Val Val Thr Pro
                85                  90                  95

Glu Glu Ile Ala Glu Asn Asn Asn Phe Leu Asp Ala Ile Leu Glu Thr
            100                 105                 110

Lys Val Met Lys Met Ala His Asp Tyr Leu Val Arg Lys Asn Gln Ala
        115                 120                 125
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Lys Pro Thr Arg Asn Asp Phe Lys Val Gln Leu Tyr Asn Ile Trp Phe
130 135 140

Gln Leu Tyr Ser Arg Ala Pro Gly Ser Arg Pro Asp Ser Cys Gly Phe
145 150 155 160

Arg His Val Phe Val Gly Glu Ser Lys Arg Gly Gln Glu Met Met Gly
165 170 175

Leu His Asn Trp Val Gln Phe Tyr Leu Gln Glu Lys Arg Lys Asn Ile
180 185 190

Asp Tyr Lys Gly Tyr Val Ala Arg Gln Asn Lys Ser Arg Pro Asp Glu
195 200 205

Asp Asp Gln Val Leu Asn Leu Gln Phe Asn Trp Lys Glu Met Val Lys
210 215 220

Pro Val Gly Ser Ser Phe Ile Gly Val Ser Pro Glu Phe Glu Phe Ala
225 230 235 240

Leu Tyr Thr Ile Val Phe Leu Ala Ser Gln Glu Lys Met Ser Arg Glu
245 250 255

Val Val Arg Leu Glu Glu Tyr Glu Leu Gln Ile Val Val Asn Arg His
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Gly Arg Tyr Ile Gly Thr Ala Tyr Pro Val Leu Leu Ser Thr Asn Asn
275 280 285

Pro Asp Leu Tyr
290

<210> 3
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic oligoribonucleotide

<220>
<221> misc_RNA
<222> (1)..(20)
<223> Synthetic oligoribonucleotide which includes U16 upstream

cleavage site

<400> 3
ggaaacguau ccuuugggag 20

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Shyntetic oligonucleotide

<220>
<221> misc_RNA
<222> (1)..(20)
<223> Mutant of SEQ ID 3

<220>
<221> variation
<222> (20)..(20)
<223> "U" is replaced by "T"

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ggaaacguau ccuugggagt 20

<210> 5
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic oligoribonucleotide

<220>
<221> misc_RNA
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<221> variation
<222> (14)..(14)
<223> "U" is replaced by "C"

<400> 5
ggaaacguau ccucugggag 20

<210> 6
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic oligoribonucleotide

<220>
<221> misc_RNA
<222> (1)..(20)
<223> Mutant of SEQ ID 3

<220>
<221> variation
<222> (14)..(14)
<223> "U" is replaced by "G"

<400> 6
ggaaacguau ccugugggag 20

<210> 7
<211> 27
<212> DNA
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<220>
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<222> (1)..(27)
<223> Primer

<400> 7
aagcttcttc atggcggctc ggccaat 27

<210> 8
<211> 20
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<223> MAHs: synthetic degenerate oligonucleotide

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<222> (1)..(20)
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<221> modified_base
<222> (6)..(6)
<223> "n" : I

<220>
<221> modified_base

<222> (18)..(18)
<223> "n" : I

<400> 8
atggcncayg aytayytngt 20

<210> 9
<211> 20
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<222> (1)..(20)
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<222> (3)..(3)
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<220>
<221> modified_base
<222> (9)..(9)
<223> "n" : I

<220>
<221> modified_base
<222> (12)..(12)
<223> "n": I

<220>
<221> modified_base
<222> (15)..(15)
<223> "n" : I

<220>
<221> modified_base
<222> (18)..(18)
<223> "n" : I

<400> 9
acnggrtang cngtnccnat 20